# Fitting von Bertalanffy Growth Models with Fixed Sex Effects

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**Load Required Packages and Data**

```
LMBL <- read.csv("Data/Clean-Data/2016_largemouth-bass_long-format.csv") %>%
    select(FID:BI.len) %>% arrange(FID, Agei)

### Making factors factors
LMBL$FID <- factor(LMBL$FID)
LMBL$Site <- factor(LMBL$Site)
LMBL$SEXCON <- factor(LMBL$SEXCON)
LMBL$Sex <- factor(LMBL$Sex)
```

```
str(LMBL)
headtail(LMBL)
```

Creating the von Bertalanffy function.

```
LVB <- function(x, Linf, K, t0) {
    y = Linf * (1 - exp(-K * (x - t0)))
    y
}
LVB <- vbFuns()


LVB(5, 422.8, 0.39, -0.4)
LVB(5, Linf = c(422.8, 0.39, -0.4))   ### Should be the same output
```

## Modeling Fixed Effects for Sex

**Lets look at the von Bertalanffy growth model fits with a fixed sex term on the parameter estimates.**

In order to fit the sex model I will have to remove the individual with no sex. In order to compare the sex model to the no sex model I will have to re-fit the no sex model without the individual with unknown sex. This means making new df excluding this individual. Then, making a new grouped data object. Finally, I will need to re-run the nlme function with out this fish to get the nlme.mod2 output.

**Removing the individual with no sex (FID=89)**

```
### Just looking at data
head(LMBL)
### Finding fish with unknown sex
(unknown.sex <- filterD(LMBL, Sex == 0))
### Getting row number for fish with the unknown sex
(FID89 <- as.numeric(row.names(LMBL[LMBL$Sex == 0, ])))
### removing the fish with unknown sex from the data set
length(LMBL$FID)   ### just seeing the number of rows in the data set
```

```
length(unique(LMBL$FID))  ### just seeing the number of fish
LMBL <- LMBL[-c(FID89), ]
length(LMBL$FID)
length(unique(LMBL$FID))  ### Good! looks like only FID 89 was removed
### Lets make sure there is no empty row in my data
LMBL <- filterD(LMBL, !is.na(FID))
### and lets just take a quick look at the data
str(LMBL)
headtail(LMBL)
```

**Remake Grouped Data Object**

```
datgr = groupedData(BI.len ~ Agei|FID, data = LMBL,
                 labels = list(x = "Age", y = "Size"),
                 units = list(x = "(Years)", y = "(mm)"))
```

**Full Sex Model, {sexmod.lkt}**

### Sex terms on all model parameters

I'm going to skip this for now it seems to be taking forever. I have this model output already converged, however, I did so with ML estimation instead of REML so I cannot compare with other model fits. I dont think this model should be used anyways since I'm not aware of a biological reason male and female largemouth bass would have a different $t_0$.

### Failed

```
sexmod.lkt <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    Sex - 1, K ~ Sex - 1, t0 ~ Sex - 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = c(389
    389.3647), K = c(0.4359, 0.4359), t0 = c(-0.3127, -0.3127))), method = "REML",
    control = list(opt = "nlminb", maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100,
        niterEM = 100))
save(sexmod.lkt, file = "model-output/sexmod.lkt.rda")
```

**{$L_\infty$, K} Sex Model, {sexmod.lk}**

I'm going to skip this for now it seems to be taking forever. I have this model output already converged, however, I did so with ML estimation instead of REML so I cannot compare with other model fits.

Unfortunaltly, I do think this is the sex model that would make the most sense biologically except for maybe the $L_\infty$ of K sex models.

### Failed

```
sexmod.lk <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    Sex - 1, K ~ Sex - 1, t0 ~ 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = c(389.3647
    389.3647), K = c(0.4359, 0.4359), t0 = -0.3127)), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
save(sexmod.lk, file = "model-output/sexmod.lk.rda")
```

### $\{L_\infty, t_0\}$ Sex Model, {sexmod.lt}

```
sexmod.lt <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    Sex - 1, K ~ 1, t0 ~ Sex - 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = c(389.3647
    389.3647), K = 0.4359, t0 = c(-0.3127, -0.3127))), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
# save(sexmod.lt, file = 'model-output/sexmod.lt.rda')
```

### $\{K, t_0\}$, Sex Model, {sexmod.kt}

```
sexmod.kt <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    1, K ~ Sex - 1, t0 ~ Sex - 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = 389.3647,
    K = c(0.4359, 0.4359), t0 = c(-0.3127, -0.3127))), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
# save(sexmod.kt, file = 'model-output/sexmod.kt.rda')
```

### $\{L_\infty\}$, Sex Model, {sexmod.l}

```
sexmod.l <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    Sex - 1, K ~ 1, t0 ~ 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = c(389.3647,
    389.3647), K = 0.4359, t0 = -0.3127)), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
# save(sexmod.l, file = 'model-output/sexmod.l.rda')
```

### $\{K\}$, Sex Model, {sexmod.k}

```
sexmod.k <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    1, K ~ Sex - 1, t0 ~ 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = 389.3647,
    K = c(0.4359, 0.4359), t0 = -0.3127)), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
# save(sexmod.k, file = 'model-output/sexmod.k.rda')
```

### $\{t_0\}$, Sex Model, {sexmod.t}

```
sexmod.t <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr, fixed = list(Linf ~
    1, K ~ 1, t0 ~ Sex - 1), random = Linf + K + t0 ~ 1, start = list(fixed = c(Linf = 389.3647,
    K = c(0.4359, 0.4359), t0 = -0.3127)), method = "REML", control = list(opt = "nlminb",
    maxIter = 1000, pnlsMaxIter = 100, msMaxIter = 100, niterEM = 100))
# save(sexmod.t, file = 'model-output/sexmod.t.rda')
```

**Zero Intercept Sex Models**

I will now try fitting the same sex models with a zero intercept (I think this is right might be slope). this is done by removing the -1 from VBPARAM ~ Sex-1 argument.

Rather than go through all of these right now which maybe I should I will just pick my favorites and go from there.

### {$L_\infty$, K} Intercept Sex Model {sexmod.lk.int}

**Failed**

```
sexmod.lk.int <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr,
                            fixed = list(Linf ~ Sex, K ~ Sex, t0 ~ 1),
                            random = Linf+K+t0 ~ 1,
                            start = list(fixed =
                                        c(Linf = c(389.3647,389.3647),
                                          K = c(0.4359,0.4359),
                                          t0 = -0.3127)),
                            method= "REML",
                            control=list(opt="nlminb",
                                        maxIter=100,
                                        pnlsMaxIter=1000,
                                        msMaxIter=100,
                                        niterEM=100))
save(sexmod.lk.int,
     file = "model-output/sexmod.lk.int.rda")
```

### {$L_\infty$} Intercept Sex Model {sexmod.l.int}

```
sexmod.l.int <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr,
                           fixed = list(Linf ~ Sex, K ~ 1, t0 ~ 1),
                           random = Linf+K+t0 ~ 1,
                           start = list(fixed =
                                       c(Linf = c(389.3647,389.3647),
                                         K = 0.4359,
                                         t0 = -0.3127)),
                           method= "REML",
                           control=list(opt="nlminb",
                                       maxIter=100,
                                       pnlsMaxIter=100,
                                       msMaxIter=100,
                                       niterEM=100))
#save(sexmod.l.int,
#     file = "model-output/sexmod.l.int.rda")
```

### {K} Intercept Sex Model {sexmod.k.int}

**Failed**

```
sexmod.k.int <- nlme::nlme(BI.len ~ LVB(Agei, Linf, K, t0), data = datgr,
                           fixed = list(Linf ~ 1, K ~ Sex, t0 ~ 1),
```

```
                                     random = Linf+K+t0 ~ 1,
                                     start = list(fixed =
                                                  c(Linf = 389.3647,
                                                    K = c(0.4359,0.4359),
                                                    t0 = -0.3127)),
                                     method= "REML",
                                     control=list(opt="nlminb",
                                                  maxIter=100,
                                                  pnlsMaxIter=1000,
                                                  msMaxIter=100,
                                                  niterEM=100))
save(sexmod.k.int,
     file = "model-output/sexmod.k.int.rda")
```

**Look at Model Fits**

```
### The outputs commented out failed to converge
load("model-output/nlme.mod2.rda")

# load('model-output/sexmod.lkt.rda') load('model-output/sexmod.lk.rda')
load("model-output/sexmod.lt.rda")
load("model-output/sexmod.kt.rda")
load("model-output/sexmod.l.rda")
load("model-output/sexmod.k.rda")
load("model-output/sexmod.t.rda")

# load('model-output/sexmod.lkt.int.rda')
# load('model-output/sexmod.lk.int.rda')
# load('model-output/sexmod.lt.int.rda')
# load('model-output/sexmod.kt.int.rda')
load("model-output/sexmod.l.int.rda")
# load('model-output/sexmod.k.int.rda')
# load('model-output/sexmod.t.int.rda')
```

**Results of $\{L_\infty\}$, Sex Model, {sexmod.l}**

```
## [1] "Iterations = 11"

## Nonlinear mixed-effects model fit by REML
##   Model: BI.len ~ LVB(Agei, Linf, K, t0)
##  Data: datgr
##        AIC      BIC     logLik
##   2809.756 2851.613 -1393.878
##
## Random effects:
##  Formula: list(Linf ~ 1, K ~ 1, t0 ~ 1)
##  Level: FID
##  Structure: General positive-definite, Log-Cholesky parametrization
##                   StdDev     Corr
## Linf.(Intercept) 60.7965255 Ln.(I) K
## K                 0.1283636 -0.880
## t0                0.4334910 -0.675  0.857
```

5

```
## Residual            4.7920294
##
## Fixed effects: list(Linf ~ Sex - 1, K ~ 1, t0 ~ 1)
##               Value Std.Error  DF  t-value p-value
## Linf.Sex1 425.4479  8.432956 208 50.45062       0
## Linf.Sex2 439.0623  8.546468 208 51.37354       0
## K           0.3855  0.015426 208 24.98993       0
## t0         -0.3887  0.043652 208 -8.90441       0
##  Correlation:
##           Lnf.S1 Lnf.S2 K
## Linf.Sex2  0.695
## K         -0.824 -0.810
## t0        -0.582 -0.543  0.811
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -1.98806932 -0.16716238  0.08612533  0.49651811  4.46707175
##
## Number of Observations: 336
## Number of Groups: 125

## Approximate 95% confidence intervals
##
##  Fixed effects:
##                  lower         est.         upper
## Linf.Sex1 408.8228527 425.4478748 442.0728969
## Linf.Sex2 422.2135142 439.0623179 455.9111216
## K           0.3550875   0.3854992   0.4159109
## t0         -0.4747482  -0.3886919  -0.3026356
## attr(,"label")
## [1] "Fixed effects:"
##
##  Random Effects:
##    Level: FID
##                             lower        est.       upper
## sd(Linf.(Intercept))    47.29589478 60.7965255 78.1509163
## sd(K)                    0.08225568  0.1283636  0.2003170
## sd(t0)                   0.36854094  0.4334910  0.5098876
## cor(Linf.(Intercept),K)  -0.95392287 -0.8799812 -0.7052801
## cor(Linf.(Intercept),t0) -0.85453505 -0.6745742 -0.3500078
## cor(K,t0)                 0.71194480  0.8565798  0.9314982
##
##  Within-group standard error:
##    lower      est.    upper
## 3.978896 4.792029 5.771337

##          numDF denDF   F-value p-value
## Linf.Sex     2   208 20992.203  <.0001
## K            1   208  3025.994  <.0001
## t0           1   208    79.289  <.0001
```
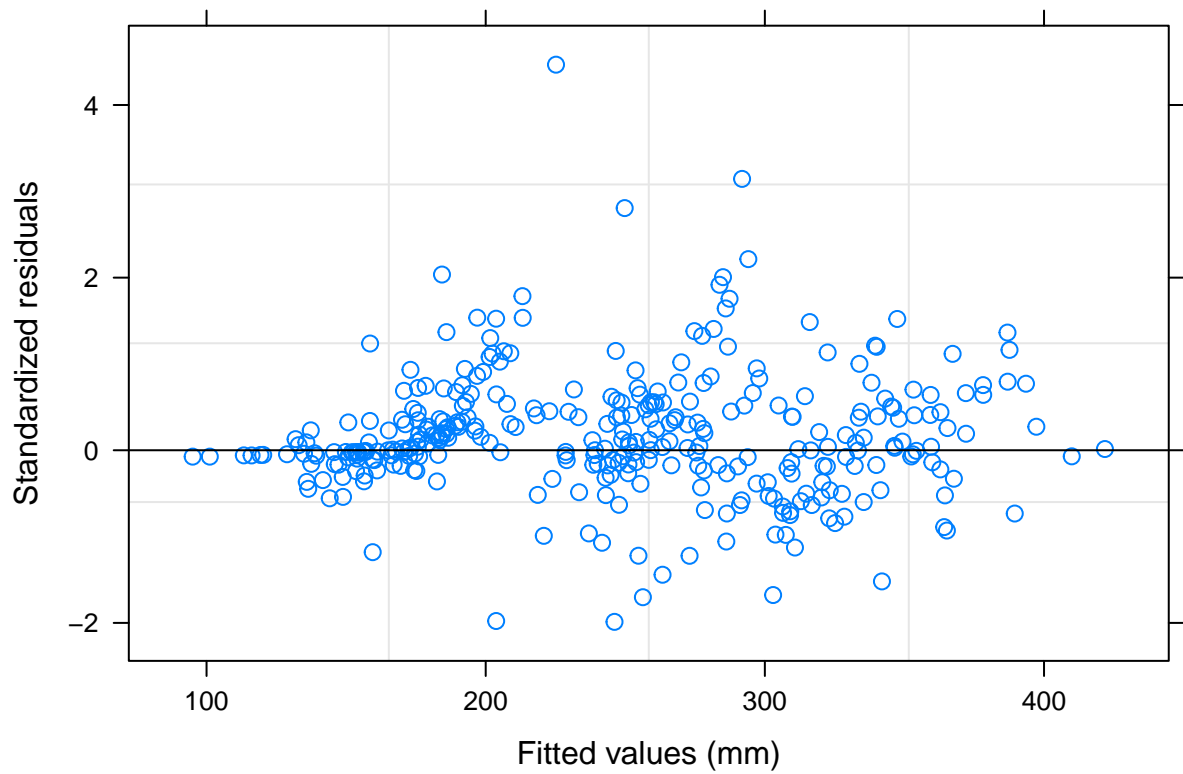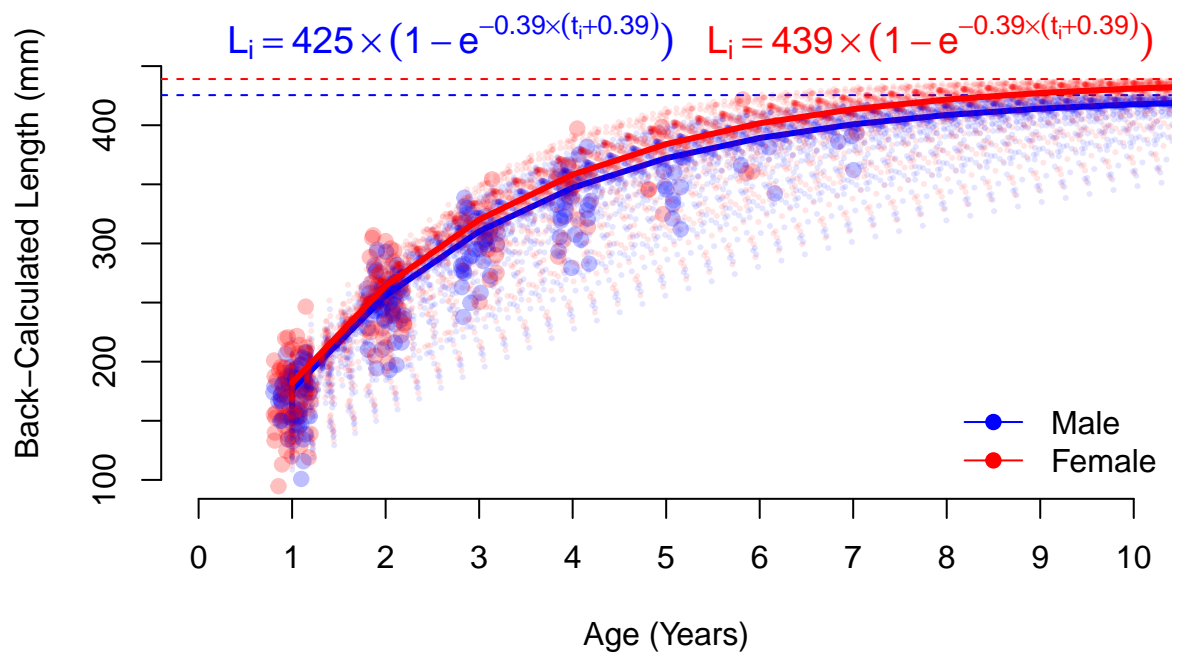
```
## expression(L[i] == 425 %*% (1 - e^{
##     -0.39 %*% (t[i] + 0.39)
## }))

## expression(L[i] == 439 %*% (1 - e^{
##     -0.39 %*% (t[i] + 0.39)
## }))
```



$$L_i = 425 \times (1 - e^{-0.39 \times (t_i + 0.39)})$$

$$L_i = 439 \times (1 - e^{-0.39 \times (t_i + 0.39)})$$

## $L_\infty$ Intercept Sex Model {sexmod.l.int}

```
## [1] "Iterations = 8"

## Nonlinear mixed-effects model fit by REML
##   Model: BI.len ~ LVB(Agei, Linf, K, t0)
##  Data: datgr
##        AIC      BIC    logLik
##   2809.756 2851.613 -1393.878
##
## Random effects:
##  Formula: list(Linf ~ 1, K ~ 1, t0 ~ 1)
##  Level: FID
##  Structure: General positive-definite, Log-Cholesky parametrization
##                  StdDev     Corr
## Linf.(Intercept) 60.7967245 Ln.(I) K
## K                 0.1283638 -0.880
## t0                0.4334913 -0.675  0.857
## Residual          4.7920262
##
## Fixed effects: list(Linf ~ Sex, K ~ 1, t0 ~ 1)
##                     Value Std.Error  DF  t-value p-value
## Linf.(Intercept) 425.4479  8.432969 208 50.45055  0.0000
## Linf.Sex2         13.6145  6.626469 208  2.05456  0.0412
## K                  0.3855  0.015426 208 24.98990  0.0000
## t0                -0.3887  0.043652 208 -8.90441  0.0000
##  Correlation:
##          Ln.(I) Lnf.S2 K
## Linf.Sex2 -0.376
## K         -0.824  0.004
## t0        -0.582  0.040  0.811
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -1.9880697 -0.1671674  0.0861218  0.4965188  4.4670194
##
## Number of Observations: 336
## Number of Groups: 125

## Approximate 95% confidence intervals
##
##  Fixed effects:
##                        lower        est.       upper
## Linf.(Intercept) 408.8228916 425.4479383 442.0729850
## Linf.Sex2          0.5508558  13.6145061  26.6781564
## K                  0.3550873   0.3854991   0.4159108
## t0                -0.4747486  -0.3886923  -0.3026359
## attr(,"label")
## [1] "Fixed effects:"
##
##  Random Effects:
##    Level: FID
##                        lower       est.      upper
## sd(Linf.(Intercept))  47.2998329 60.7967245 78.1449211
## sd(K)                  0.0822892  0.1283638  0.2002362
```
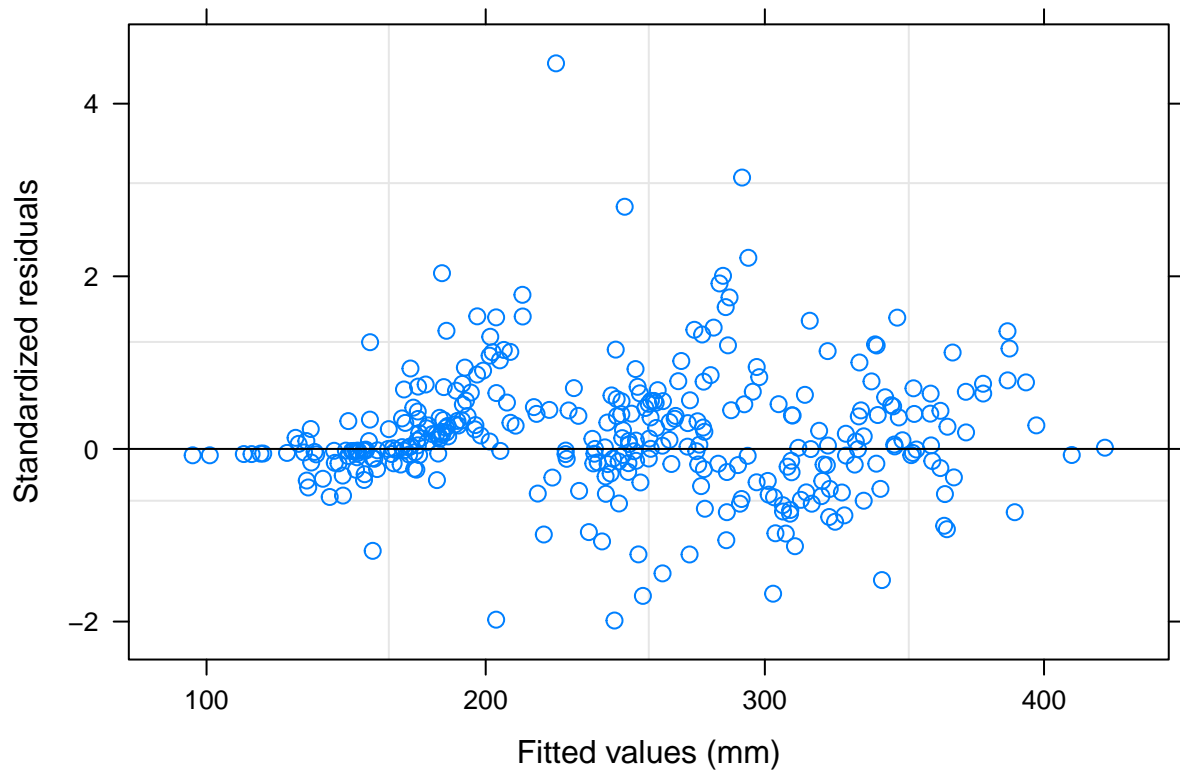
8

```
## sd(t0)                      0.3685501  0.4334913  0.5098757
## cor(Linf.(Intercept),K)    -0.9538721 -0.8799822 -0.7055677
## cor(Linf.(Intercept),t0)   -0.8543408 -0.6745775 -0.3506498
## cor(K,t0)                    0.7122032  0.8565806  0.9314297
##
##  Within-group standard error:
##    lower      est.     upper
## 3.979148 4.792026 5.770963

##                  numDF denDF  F-value p-value
## Linf.(Intercept)     1   208 41958.70  <.0001
## Linf.Sex             1   208    25.59  <.0001
## K                    1   208  3026.00  <.0001
## t0                   1   208    79.29  <.0001
```



```
fixef(sexmod.l.int)
ranef(sexmod.l.int)
coef(sexmod.l.int)[1,3]
```

**Comparing Models**

```
AIC(nlme.mod2, sexmod.lt, sexmod.kt, sexmod.l, sexmod.k, sexmod.t, sexmod.l.int)
```

```
## Warning in AIC.default(nlme.mod2, sexmod.lt, sexmod.kt, sexmod.l,
## sexmod.k, : models are not all fitted to the same number of observations
```

```
##                df      AIC
## nlme.mod2      10 2825.199
## sexmod.lt      12 2827.788
## sexmod.kt      12 2837.204
## sexmod.l       11 2809.756
## sexmod.k       11 2824.301
## sexmod.t       11 2829.548
## sexmod.l.int   11 2809.756
```

```
BIC(nlme.mod2, sexmod.lt, sexmod.kt, sexmod.l, sexmod.k, sexmod.t, sexmod.l.int)
```

```
## Warning in BIC.default(nlme.mod2, sexmod.lt, sexmod.kt, sexmod.l,
## sexmod.k, : models are not all fitted to the same number of observations
```

```
##                df      BIC
## nlme.mod2      10 2863.280
## sexmod.lt      12 2873.413
## sexmod.kt      12 2882.830
## sexmod.l       11 2851.613
## sexmod.k       11 2866.158
## sexmod.t       11 2871.404
## sexmod.l.int   11 2851.613
```

```
anova(nlme.mod2, sexmod.lt, sexmod.kt, sexmod.l, sexmod.k, sexmod.t, sexmod.l.int)
```

```
##              Model df      AIC      BIC    logLik    Test   L.Ratio p-value
## nlme.mod2        1 10 2825.199 2863.280 -1402.599
## sexmod.lt        2 12 2827.788 2873.413 -1401.894 1 vs 2  1.410824  0.4939
## sexmod.kt        3 12 2837.204 2882.830 -1406.602
## sexmod.l         4 11 2809.756 2851.613 -1393.878 3 vs 4 25.448099  <.0001
## sexmod.k         5 11 2824.301 2866.157 -1401.150
## sexmod.t         6 11 2829.548 2871.404 -1403.774
## sexmod.l.int     7 11 2809.756 2851.613 -1393.878
```

```
anova(nlme.mod2, sexmod.l, sexmod.l.int)
```

```
##              Model df      AIC      BIC    logLik    Test L.Ratio p-value
## nlme.mod2        1 10 2825.199 2863.280 -1402.599
## sexmod.l         2 11 2809.756 2851.613 -1393.878 1 vs 2 17.4423  <.0001
## sexmod.l.int     3 11 2809.756 2851.613 -1393.878
```

```
anova(sexmod.l, nlme.mod2, sexmod.l.int)
```

```
##              Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## sexmod.l         1 11 2809.756 2851.613 -1393.878
## nlme.mod2        2 10 2825.199 2863.280 -1402.599 1 vs 2 17.44230  <.0001
## sexmod.l.int     3 11 2809.756 2851.613 -1393.878 2 vs 3 17.44229  <.0001
```

```
anova(sexmod.l, sexmod.k, nlme.mod2)
```

```
##            Model df      AIC      BIC    logLik    Test L.Ratio p-value
## sexmod.l       1 11 2809.756 2851.613 -1393.878
```

```
## sexmod.k      2 11 2824.301 2866.157 -1401.150
## nlme.mod2     3 10 2825.199 2863.280 -1402.599 2 vs 3 2.89759  0.0887
```

## $\{L_\infty\}$ Sex Model vs. No Sex Model (sexmod.l vs. nlme.mod2)

```
anova(sexmod.l, nlme.mod2)
```

```
##             Model df     AIC      BIC    logLik   Test L.Ratio p-value
## sexmod.l       1 11 2809.756 2851.613 -1393.878
## nlme.mod2      2 10 2825.199 2863.280 -1402.599 1 vs 2 17.4423  <.0001
```
```
anova(nlme.mod2, sexmod.l)
```

```
##             Model df     AIC      BIC    logLik   Test L.Ratio p-value
## nlme.mod2      1 10 2825.199 2863.280 -1402.599
## sexmod.l       2 11 2809.756 2851.613 -1393.878 1 vs 2 17.4423  <.0001
```

There is a significant difference between the nlme.mod2 and sexmod.l with sexmod.l being the model that best describes the data (loglikliehood,df=11, L Ratio = 17.4423, p<0.0001).

## $\{L_\infty\}$ Sex Model vs. $\{L_\infty\}$ Intercept Sex Model (sexmod.l vs. sexmod.l.int)

```
anova(sexmod.l, sexmod.l.int)
```

```
##               Model df     AIC      BIC    logLik
## sexmod.l         1 11 2809.756 2851.613 -1393.878
## sexmod.l.int     2 11 2809.756 2851.613 -1393.878
```
```
anova(sexmod.l.int, sexmod.l)
```

```
##               Model df     AIC      BIC    logLik
## sexmod.l.int     1 11 2809.756 2851.613 -1393.878
## sexmod.l         2 11 2809.756 2851.613 -1393.878
```

Estimates for the von Bertalanffy growth parameters were obtained from 336 obsercations of 125 largemouth bass. Two additional fish were removed prior to model fitting due to inaccurate or incomplete data. The von Bertalanffy growth model fit with a sex term on the $L_\infty$ described the data better than when no sex term was used (Likelihood Ratio Test, Liklihood Ratio = 17, df = 11, p < 0.0001). The maximum asymptotic length ($L_\infty$) was larger for female largemouth bass ($L_\infty = 439$, SE = 8.55) than male largemouth bass ($L_\infty = 425$, SE = 8.43) ($F_{2,208} = 20992$, p < 0.001). The brody growth rate coefficient (K) and the theoretical time at which length was zero ($t_0$) were fit without sex effects as 0.39 (SE = 0.015) and -0.39 (SE = 0.044) respectively.

| Sex | Number of Individuals | Number of Observations |
|---|---|---|
| Male | 56 | 179 |
| Female | 69 | 157 |
| Total | 125 | 336 |